

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> A new aminopeptidase and the gene encoding the peptidase

<130> Y1J0140

<150> JP 2001-78930

<151> 2001-03-19

<150> JP 2001-293348

<151> 2001-09-26

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Aspergillus nidulans

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<212> DNA

<213> Aspergillus nidulans

<220>

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<222> (72)..(1628)

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Met Ala Lys Lys Ile Leu Ser Asp Ile His His His Glu

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10

tct aac ttg gct tac cgc cag tat gcc cag ctg cct gaa acc ctc cac 158

Ser Asn Leu Ala Tyr Arg Gln Tyr Ala Gln Leu Pro Glu Thr Leu His

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25

ctc aac tac cag cct cct act gct act gca acc ccc gcc gca cac acc 206

Leu Asn Tyr Gln Pro Pro Thr Ala Thr Ala Thr Pro Ala Ala His Thr

30

35

40

45

agc ccg atc cca gag gca atc aac ccc gac gat tac tcg cag gct tac 254

Ser Pro Ile Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr

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55

60

tgc gat ttt atg act gag cat ccc acc att ttt cac gca gtc gat ggc 302

Cys Asp Phe Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly

65

70

75

ttc tct aag caa ctc gaa agc aag gga tac aag tac cta tcc gag cgg 350
Phe Ser Lys Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg

80

85

90

gaa tta tgg acg ccg cag ctc aaa cgc gga gga aag tac tat acg act 398
Glu Leu Trp Thr Pro Gln Leu Lys Arg Gly Gly Lys Tyr Tyr Thr Thr

95

100

105

cgc aat gga agc tcg ttg att gcg ttc tct gtc ggc ccc gag tat aag 446
Arg Asn Gly Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys
110 115 120 125

agt ggg aat ggc ctc gct atc atc gcc ggc cac att gat gcc ctc acg 494
Ser Gly Asn Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr
130 135 140

gcg aag ctc aag ccc gtc tca aaa ctt ccc aat aaa gct gga tac att 542
Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile
145 150 155

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Gln Met Gly Val Ala Pro Tyr Ala Gly Gly Leu Gly Lys Thr Trp Trp
160 165 170

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Asp Arg Asp Leu Ser Ile Gly Gly Lys Val Leu Val Arg Asn Ala Ser
175 180 185

acc ggc aag gtt gaa tcc aag cta gtc aag ttg aac tgg ccg att gct 686

Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asn Trp Pro Ile Ala	
190	205
cgc atc cca acg cta gcc gaa cac ttt ggc gct cct tcg cag ggg cca	734
Arg Ile Pro Thr Leu Ala Glu His Phe Gly Ala Pro Ser Gln Gly Pro	
210	220
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Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn Ser	
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Asp Leu Phe Gln Ser Thr Thr Pro Ala Ala Asp Glu Gly Ile Glu Pro	
240	250
ggc acc ttt gcc tct acg cag ccc cca aaa ctc atc aaa gtg atc tcc	878
Gly Thr Phe Ala Ser Thr Gln Pro Pro Lys Leu Ile Lys Val Ile Ser	
255	265
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Lys Glu Leu Gly Ile Thr Asn Tyr Ser Ser Ile Leu Ser Trp Glu Leu	
270	285
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Glu Leu Tyr Asp Ser Gln Pro Ala Arg Ile Gly Gly Ile Asp Lys Asp	
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Phe Ile Phe Ala Gly Arg Ile Asp Asp Lys Leu Cys Cys Tyr Ala Ala	

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320	325	330	
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Lys Met Val Gly Tyr Phe Asp Asp Glu Glu Ile Gly Ser Leu Leu Arg			
335	340	345	
cag ggt gcc cgc tcc aac ttc atg tct agc gtc atc gaa cgc att gca			1166
Gln Gly Ala Arg Ser Asn Phe Met Ser Ser Val Ile Glu Arg Ile Ala			
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caa tcc ttt gca aca tca tat gga ccc gat ctc ctt gcc caa acc gtt			1214
Gln Ser Phe Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val			
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gca aag agc ttc ctt atc tct tct gat gtc atc cac gct gtc aat ccc			1262
Ala Lys Ser Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro			
385	390	395	
aac ttc ttg aat gtc tat ctc gag aac cac gcg cct cgt ctc aat gtc			1310
Asn Phe Leu Asn Val Tyr Leu Glu Asn His Ala Pro Arg Leu Asn Val			
400	405	410	
ggc gtc tcc gtc tcc gca gac tca aac ggc cac atg act acc gac agt			1358
Gly Val Ser Val Ser Ala Asp Ser Asn Gly His Met Thr Thr Asp Ser			
415	420	425	

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 Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln
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ggg ccc atg acc agc tcg cgg att gga atg agg gcc att gat gtc ggt 1502
 Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly
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atc cca cag ttg agc atg cat agc att cgc gcc acc aca ggg agt cgc 1550
 Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg
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 Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe Phe Asp Tyr Phe
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<211> 519

<212> PRT

<213> Aspergillus nidulans

<400> 3

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35 40 45

Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr Cys Asp Phe

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Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly Phe Ser Lys

65 70 75 80

Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg Glu Leu Trp

	85	90	95
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Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys Ser Gly Asn			
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Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr Ala Lys Leu			
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Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile Gln Met Gly			
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Val Ala Pro Tyr Ala Gly Gly Leu Gly Lys Thr Trp Trp Asp Arg Asp			
	165	170	175
Leu Ser Ile Gly Gly Lys Val Leu Val Arg Asn Ala Ser Thr Gly Lys			
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Val Glu Ser Lys Leu Val Lys Leu Asn Trp Pro Ile Ala Arg Ile Pro			
	195	200	205
Thr Leu Ala Glu His Phe Gly Ala Pro Ser Gln Gly Pro Phe Asn Lys			
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Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn Ser Asp Leu Phe			
	225	230	235
			240

Gln Ser Thr Thr Pro Ala Ala Asp Glu Gly Ile Glu Pro Gly Thr Phe
245 250 255

Ala Ser Thr Gln Pro Pro Lys Leu Ile Lys Val Ile Ser Lys Glu Leu
260 265 270

Gly Ile Thr Asn Tyr Ser Ser Ile Leu Ser Trp Glu Leu Glu Leu Tyr
275 280 285

Asp Ser Gln Pro Ala Arg Ile Gly Gly Ile Asp Lys Asp Phe Ile Phe
290 295 300

Ala Gly Arg Ile Asp Asp Lys Leu Cys Cys Tyr Ala Ala Gln Glu Ala
305 310 315 320

Leu Met Ala Thr Ser Asp His Thr Ser Pro Ser Ser Ile Lys Met Val
325 330 335

Gly Tyr Phe Asp Asp Glu Glu Ile Gly Ser Leu Leu Arg Gln Gly Ala
340 345 350

Arg Ser Asn Phe Met Ser Ser Val Ile Glu Arg Ile Ala Gln Ser Phe
355 360 365

Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val Ala Lys Ser
370 375 380

Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro Asn Phe Leu
385 390 395 400

Asn Val Tyr Leu Glu Asn His Ala Pro Arg Leu Asn Val Gly Val Ser
405 410 415

Val Ser Ala Asp Ser Asn Gly His Met Thr Thr Asp Ser Val Ser Tyr
420 425 430

Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln Leu Gln Val
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Phe Gln Ile Arg Asn Asp Ser Arg Ser Gly Gly Thr Ile Gly Pro Met
450 455 460

Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly Ile Pro Gln
465 470 475 480

Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg Asp Pro Gly
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<212> DNA

<213> *Aspergillus oryzae*

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<222> (73)..(1602)

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Met Thr Lys Arg Ser Val Leu Asp Leu Arg Asp Ser Ala

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atg gct tat cgc ctg tcg gcc cag ctt cct gag ccc tcc cca gcc acc 159

Met Ala Tyr Arg Leu Ser Ala Gln Leu Pro Glu Pro Ser Pro Ala Thr

15

20

25

att gca acc cca gtg gcg agg agt ggc ccc ttc gcc ccg gaa gat tac 207

Ile Ala Thr Pro Val Ala Arg Ser Gly Pro Phe Ala Pro Glu Asp Tyr

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35

40

45

acg aaa cca tac tgc gaa ttc atg aca gca aac ccc aca atc ttt cac 255

Thr Lys Pro Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His

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Ala Val Asp Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg

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ctt ccc gag cgc gag acg tgg aac tcc aag tta gag aag ggt ggg aag 351
 Leu Pro Glu Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys
 80 85 90

tac tac gtc act cgg aat ggt agt gct ttc atc tca ttc tca att gga 399
 Tyr Tyr Val Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly
 95 100 105

aga gat tat aaa agt ggc aat gga atg gcc att gtt gca ggt cat atc 447
 Arg Asp Tyr Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile
 110 115 120 125

gat gca ctc acc gcc aaa ttg aag ccc gtg tcc aag ctg ccc aac aag 495
 Asp Ala Leu Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys
 130 135 140

gct ggc ttt tcc cag ctc gga gtt gcg ccc tac gca ggc gct ctg agt 543
 Ala Gly Phe Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser
 145 150 155

gac aca tgg tgg gac cgc gat ctc tca ata ggt ggc cgt gtt ctg gtc 591
 Asp Thr Trp Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val
 160 165 170

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 Gln Asp Ser Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp
 175 180 185

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Trp Pro Ile Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro	
190 195 200 205	
tcg caa ggc ccc ttc aac aaa gag act cag atg gtg cct ata att ggc	735
Ser Gln Gly Pro Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly	
210 215 220	
gtt gat aac tcc gat ctt ttc cag cag caa gcc cca tcc aag ata gat	783
Val Asp Asn Ser Asp Leu Phe Gln Gln Gln Ala Pro Ser Lys Ile Asp	
225 230 235	
caa gac aac ggg atc aaa cct ggt aca ttt gca gcc acg caa ccg gaa	831
Gln Asp Asn Gly Ile Lys Pro Gly Thr Phe Ala Ala Thr Gln Pro Glu	
240 245 250	
aag ctt gtc aaa gtc ata tcc aag gag ctt ggt atc aca gac tac agc	879
Lys Leu Val Lys Val Ile Ser Lys Glu Leu Gly Ile Thr Asp Tyr Ser	
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tcg att ata agc tgg gag ctg gag ctg tat gac agt caa cca gca caa	927
Ser Ile Ile Ser Trp Glu Leu Glu Leu Tyr Asp Ser Gln Pro Ala Gln	
270 275 280 285	
gtt ggt ggc ctg gac aag gac ctg att ttt gct ggt cgc att gac gat	975
Val Gly Gly Leu Asp Lys Asp Leu Ile Phe Ala Gly Arg Ile Asp Asp	
290 295 300	
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Lys Leu Cys Cys Tyr Ala Ala Gln Glu Ala Leu Leu Ala Ser Ser Asp	
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Ser Thr Ser Thr Ser Ser Ile Lys Met Val Gly Met Phe Asp Asp Glu	
320	325 330
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Glu Ile Gly Ser Leu Leu Arg Gln Gly Ala Arg Ser Asn Phe Met Ser	
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Ser Val Ile Glu Arg Ile Thr Glu Ala Phe Ser Pro Asn Tyr Gly Pro	
350	355 360 365
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Asn Val Leu Ser Gln Thr Val Ala Asn Ser Phe Phe Val Ser Ser Asp	
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gtc atc cat gcg gtc aat ccg aac ttc ctt ggt gtc tat ctt gag aac	1263
Val Ile His Ala Val Asn Pro Asn Phe Leu Gly Val Tyr Leu Glu Asn	
385	390 395
cat gct ccc cgt ctg aac gtc ggt gtg gcc gtc tcg gct gac tct aac	1311
His Ala Pro Arg Leu Asn Val Gly Val Ala Val Ser Ala Asp Ser Asn	
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ggc cat atg aca aca gac agt gtg agc tac gga ttc atc aag cgt gtc	1359
Gly His Met Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val	

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Ala Asp Arg Cys Gly Ser Thr Leu Gln Val Phe Gln Ile Arg Asn Asp			
430	435	440	445
tcc cgt agt ggc ggg act att gga ccc atg acc agt tct cgc att ggc			1455
Ser Arg Ser Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly			
	450	455	460
atg agg gcc att gac gtg ggg atc ccg cag ttg agt atg cac agt atc			1503
Met Arg Ala Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile			
	465	470	475
cgt gcg act acc ggt agt ttg gat ccg gga ttg ggt gtg aag ctg ttc			1551
Arg Ala Thr Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe			
	480	485	490
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Lys Gly Phe Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp			
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ttc tgatgcgctc ctctggaata ctaggaaatg tttccatcga taagtatgca			1652
Phe			
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<212> PRT

<213> *Aspergillus oryzae*

<400> 5

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35 40 45

Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His Ala Val Asp

50 55 60

Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg Leu Pro Glu

65 70 75 80

Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys Tyr Tyr Val

85 90 95

Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly Arg Asp Tyr

100 105 110

Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile Asp Ala Leu

115 120 125

Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Phe
130 135 140

Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser Asp Thr Trp
145 150 155 160

Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val Gln Asp Ser
165 170 175

Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp Trp Pro Ile
180 185 190

Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro Ser Gln Gly
195 200 205

Pro Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn
210 215 220

Ser Asp Leu Phe Gln Gln Gln Ala Pro Ser Lys Ile Asp Gln Asp Asn
225 230 235 240

Gly Ile Lys Pro Gly Thr Phe Ala Ala Thr Gln Pro Glu Lys Leu Val
245 250 255

Lys Val Ile Ser Lys Glu Leu Gly Ile Thr Asp Tyr Ser Ser Ile Ile
260 265 270

Ser Trp Glu Leu Glu Leu Tyr Asp Ser Gln Pro Ala Gln Val Gly Gly

275	280	285
Leu Asp Lys Asp Leu Ile Phe Ala Gly Arg Ile Asp Asp Lys Leu Cys		
290	295	300
Cys Tyr Ala Ala Gln Glu Ala Leu Leu Ala Ser Ser Asp Ser Thr Ser		
305	310	315
Thr Ser Ser Ile Lys Met Val Gly Met Phe Asp Asp Glu Glu Ile Gly		
	325	330
		335
Ser Leu Leu Arg Gln Gly Ala Arg Ser Asn Phe Met Ser Ser Val Ile		
	340	345
		350
Glu Arg Ile Thr Glu Ala Phe Ser Pro Asn Tyr Gly Pro Asn Val Leu		
	355	360
		365
Ser Gln Thr Val Ala Asn Ser Phe Phe Val Ser Ser Asp Val Ile His		
	370	375
		380
Ala Val Asn Pro Asn Phe Leu Gly Val Tyr Leu Glu Asn His Ala Pro		
385	390	395
		400
Arg Leu Asn Val Gly Val Ala Val Ser Ala Asp Ser Asn Gly His Met		
	405	410
		415
Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Asp Arg		
	420	425
		430

Cys Gly Ser Thr Leu Gln Val Phe Gln Ile Arg Asn Asp Ser Arg Ser
435 440 445

Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala
450 455 460

Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr
465 470 475 480

Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe
485 490 495

Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp Phe
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